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P#12



1645

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,309A

DATE: 04/03/2002 P.5

TIME: 11:11:01

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF3\04032002\I647309A.raw

3 <110> APPLICANT: Pierre Fabre Medicament
 5 <120> TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
 7 <130> FILE REFERENCE: D17064
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/647,309A
 C--> 10 <141> CURRENT FILING DATE: 2002-02-28
 12 <150> PRIOR APPLICATION NUMBER: FR 98 03814
 13 <151> PRIOR FILING DATE: 1998-03-27
 15 <160> NUMBER OF SEQ ID NOS: 136
 17 <170> SOFTWARE: PatentIn Vers. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1032
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Klebsiella pneumoniae
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1032)
 27 <223> OTHER INFORMATION: rP40
 29 <400> SEQUENCE: 1

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31	Met	Lys	Ala	Ile	Phe	Val	Leu	Asn	Ala	Ala	Pro	Lys	Asp	Asn	Thr	Trp	
32	1				5				10					15			
34	tat	gca	ggt	ggt	aaa	ctg	ggt	tgg	tcc	cag	tat	cac	gac	acc	ggt	ttc	96
35	Tyr	Ala	Gly	Gly	Lys	Leu	Gly	Trp	Ser	Gln	Tyr	His	Asp	Thr	Gly	Phe	
36					20				25					30			
38	tac	ggt	aac	ggt	ttc	cag	aac	aac	aac	ggt	ccg	acc	cgt	aac	gat	cag	144
39	Tyr	Gly	Asn	Gly	Phe	Gln	Asn	Asn	Asn	Gly	Pro	Thr	Arg	Asn	Asp	Gln	
40			35					40				45					
42	ctt	ggt	gct	ggt	gcg	ttc	ggt	ggt	tac	cag	ggt	aac	ccg	tac	ctc	ggt	192
43	Leu	Gly	Ala	Gly	Ala	Phe	Gly	Gly	Tyr	Gln	Val	Asn	Pro	Tyr	Leu	Gly	
44		50				55			60								
46	ttc	gaa	atg	ggt	tat	gac	tgg	ctg	ggc	cgt	atg	gca	tat	aaa	ggc	agc	240
47	Phe	Glu	Met	Gly	Tyr	Asp	Trp	Leu	Gly	Arg	Met	Ala	Tyr	Lys	Gly	Ser	
48	65				70				75					80			
50	ggt	gac	aac	ggt	gct	ttc	aaa	gct	cag	ggc	ggt	cag	ctg	acc	gct	aaa	288
51	Val	Asp	Asn	Gly	Ala	Phe	Lys	Ala	Gln	Gly	Val	Gln	Leu	Thr	Ala	Lys	
52					85				90					95			
54	ctg	ggt	tac	ccg	atc	act	gac	gat	ctg	gac	atc	tac	acc	cgt	ctg	ggc	336
55	Leu	Gly	Tyr	Pro	Ile	Thr	Asp	Asp	Leu	Asp	Ile	Tyr	Thr	Arg	Leu	Gly	
56				100					105					110			
58	ggc	atg	ggt	tgg	cgc	gct	gac	tcc	aaa	ggc	aac	tac	gct	tct	acc	ggc	384
59	Gly	Met	Val	Trp	Arg	Ala	Asp	Ser	Lys	Gly	Asn	Tyr	Ala	Ser	Thr	Gly	
60					115				120					125			
62	ggt	tcc	cgt	agc	gaa	cac	gac	act	ggc	ggt	tcc	cca	gta	ttt	gct	ggc	432

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DATE: 04/03/2002

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Input Set : N:\EBONY'S\EP.txt

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63 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
64      130      135      140
66 ggc gta gag tgg gct gtt act cgt gac atc gct acc cgt ctg gaa tac 480
67 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
68 145      150      155      160
70 cag tgg gtt aac aac atc ggc gac gcg ggc act gtg ggt acc cgt cct 528
71 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
72      165      170      175
74 gat aac ggc atg ctg agc ctg ggc gtt tcc tac cgc ttc ggt cag gaa 576
75 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
76      180      185      190
78 gat gct gca ccg gtt gtt gct ccg gct ccg gct ccg gct ccg gaa gtg 624
79 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
80      195      200      205
82 gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac 672
83 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
84      210      215      220
86 aaa gct acc ctg aaa ccg gaa ggt cag cag gct ctg gat cag ctg tac 720
87 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
88 225      230      235      240
90 act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg 768
91 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
92      245      250      255
94 ggc tac acc gac cgc atc ggt tcc gaa gct tac aac cag cag ctg tct 816
95 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
96      260      265      270
98 gag aaa cgt gct cag tcc gtc gtt gac tac ctg gtt gct aaa ggc atc 864
99 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
100      275      280      285
102 ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt 912
103 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
104      290      295      300
106 act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat 960
107 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
108 305      310      315      320
110 tgc ctg gct ccg gat cgt cgt gta gag atc gaa gtt aaa ggc tac aaa 1008
111 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
112      325      330      335
114 gaa gtt gta act cag cct cag gct 1032
115 Glu Val Val Thr Gln Pro Gln Ala
116      340
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 344
121 <212> TYPE: PRT
122 <213> ORGANISM: Klebsiella pneumoniae
124 <400> SEQUENCE: 2
125 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
126 1      5      10      15
128 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe

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RAW SEQUENCE LISTING

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Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF3\04032002\I647309A.raw

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129          20          25          30
131 Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
132          35          40          45
134 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
135          50          55          60
137 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
138 65          70          75          80
140 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
141          85          90          95
143 Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
144          100          105          110
146 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
147          115          120          125
149 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
150          130          135          140
152 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
153 145          150          155          160
155 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
156          165          170          175
158 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
159          180          185          190
161 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Glu Val
162          195          200          205
164 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
165          210          215          220
167 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
168 225          230          235          240
170 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
171          245          250          255
173 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
174          260          265          270
176 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
177          275          280          285
179 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
180          290          295          300
182 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
183 305          310          315          320
185 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
186          325          330          335
188 Glu Val Val Thr Gln Pro Gln Ala
189          340
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 303
194 <212> TYPE: DNA
195 <213> ORGANISM: Respiratory Syncytial Virus (RSV)
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (1)-(303)
201 <220> FEATURE:

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RAW SEQUENCE LISTING

DATE: 04/03/2002

PATENT APPLICATION: US/09/647,309A

TIME: 11:11:01

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF3\04032002\I647309A.raw

202 <223> OTHER INFORMATION: G2A

204 <400> SEQUENCE: 3

205 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa 48

206 Thr Val Lys Thr Lys Asn Thr Thr Thr Gln Thr Gln Pro Ser Lys

207 1 5 10 15

209 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac 96

210 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn

211 20 25 30

213 gat ttc cat ttc gaa gtg ttc aac ttc gtg ccg tgc agc atc tgc agc 144

214 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser

215 35 40 45

217 aac aac ccg acc tgc tgg gcg atc tgc aaa cgt atc ccg aac aaa aaa 192

218 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys

219 50 55 60

221 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa 240

222 Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys

223 65 70 75 80

225 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg 288

226 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val

227 85 90 95

229 ccg acc acc aaa ccg 303

230 Pro Thr Thr Lys Pro

231 100

234 <210> SEQ ID NO: 4

235 <211> LENGTH: 101

236 <212> TYPE: PRT

237 <213> ORGANISM: Respiratory Syncytial Virus (RSV)

239 <400> SEQUENCE: 4

240 Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser Lys

241 1 5 10 15

243 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn

244 20 25 30

246 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser

247 35 40 45

249 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys

250 50 55 60

252 Pro Gly Lys Lys Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys

253 65 70 75 80

255 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val

256 85 90 95

258 Pro Thr Thr Lys Pro

259 100

262 <210> SEQ ID NO: 5

263 <211> LENGTH: 303

264 <212> TYPE: DNA

265 <213> ORGANISM: Respiratory Syncytial Virus (RSV)

267 <220> FEATURE:

268 <221> NAME/KEY: CDS

269 <222> LOCATION: (1)..(303)

RAW SEQUENCE LISTING

DATE: 04/03/2002

PATENT APPLICATION: US/09/647,309A

TIME: 11:11:01

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF3\04032002\I647309A.raw

271 <220> FEATURE:

272 <223> OTHER INFORMATION: G2B

274 <400> SEQUENCE: 5

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276 Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr Asn Lys
277   1          5          10          15
279 ccg agc acc aaa agc cgt agc aaa aac ccg ccg aaa aaa ccg aaa gat      96
280 Pro Ser Thr Lys Ser Arg Ser Lys Asn Pro Pro Lys Lys Pro Lys Asp
281          20          25          30
283 gat tac cac ttc gaa gtg ttc aac ttc gtg ccc tgc agc atc tgc ggc      144
284 Asp Tyr His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Gly
285          35          40          45
287 aac aac cag ctg tgc aaa agc atc tgc aaa acc atc ccg agc aac aaa      192
288 Asn Asn Gln Leu Cys Lys Ser Ile Cys Lys Thr Ile Pro Ser Asn Lys
289          50          55          60
291 ccg aaa aag aaa ccg acc atc aaa ccg acc aac aaa ccg acc acc aaa      240
292 Pro Lys Lys Lys Pro Thr Ile Lys Pro Thr Asn Lys Pro Thr Thr Lys
293   65          70          75          80
295 acc acc aac aaa cgt gat ccg aaa acc ccg gcg aaa atg ccg aag aag      288
296 Thr Thr Asn Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Pro Lys Lys
297          85          90          95
299 gaa atc atc acc aac
300 Glu Ile Ile Thr Asn
301          100

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304 <210> SEQ ID NO: 6

305 <211> LENGTH: 101

306 <212> TYPE: PRT

307 <213> ORGANISM: Respiratory Syncytial Virus (RSV)

309 <400> SEQUENCE: 6

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310 Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr Asn Lys
311   1          5          10          15
313 Pro Ser Thr Lys Ser Arg Ser Lys Asn Pro Pro Lys Lys Pro Lys Asp
314          20          25          30
316 Asp Tyr His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Gly
317          35          40          45
319 Asn Asn Gln Leu Cys Lys Ser Ile Cys Lys Thr Ile Pro Ser Asn Lys
320          50          55          60
322 Pro Lys Lys Lys Pro Thr Ile Lys Pro Thr Asn Lys Pro Thr Thr Lys
323   65          70          75          80
325 Thr Thr Asn Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Pro Lys Lys
326          85          90          95
328 Glu Ile Ile Thr Asn
329          100

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332 <210> SEQ ID NO: 7

333 <211> LENGTH: 303

334 <212> TYPE: DNA

335 <213> ORGANISM: Respiratory Syncytial Virus (RSV)

337 <220> FEATURE:

338 <221> NAME/KEY: CDS

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 04/03/2002

PATENT APPLICATION: US/09/647,309A

TIME: 11:11:02

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF3\04032002\I647309A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:621 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:621 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:638 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:638 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:655 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:655 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:882 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:882 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:902 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:902 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:922 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:922 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:942 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:942 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:3222 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:129
L:3222 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129
L:3222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129
L:3242 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:130
L:3242 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:130
L:3242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130
L:3321 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:135
L:3321 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135
L:3321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135
L:3338 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:136
L:3338 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136
L:3338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136